



SEQUENCE LISTING

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1

<110> Blundell, Tom L  
Abell, Christopher  
Inoue, Tsuyoshi  
von Delft, Frank

<120> Crystal Structure

<130> 620-139

<140> US 09/820,745

<141> 2001-03-30

<160> 12

<170> PatentIn Ver. 2.1

<210> 1

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 1

Leu Val Gly Asp Ser Leu Gly Met

1

5

<210> 2

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 2

Val Lys Ile Glu Gly Gly

1

5

<210> 3

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Conserved  
sequence motif

<220>  
<221> SITE  
<222> (3)  
<223> Xaa is a hydrophobic residue

<400> 3  
Gly His Xaa Gly Leu Thr Pro Gln  
1 5

<210> 4  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 4  
Gly Gly Tyr Lys Val Gln Gly  
1 5

<210> 5  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 5  
Ile Gly Ile Gly Ala Gly  
1 5

<210> 6  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Conserved  
sequence motif

<400> 6  
Asp Gly Asn Ile Leu Val  
1 5

<400> 7

Lys Arg Phe Ala Thr Ile Thr Ala Tyr Asp Tyr Ser Phe Ala Lys Leu  
20 25 30

Phe Ala Asp Glu Gly Leu Asn Val Met Leu Val Gly Asp Ser Leu Gly  
35 40 45

Met Thr Val Gln Gly His Asp Ser Thr Leu Pro Val Thr Val Ala Asp  
50 55 60

Ile Ala Tyr His Thr Ala Ala Val Arg Arg Gly Ala Pro Asn Cys Leu  
65 70 75 80

Leu Leu Ala Asp Leu Pro Phe Met Ala Tyr Ala Thr Pro Glu Gln Ala  
85 90 95

Phe Glu Asn Ala Ala Thr Val Met Arg Ala Gly Ala Asn Met Val Lys  
100 105 110

Ile Glu Gly Gly Glu Trp Leu Val Glu Thr Val Gln Met Leu Thr Glu  
115 120 125

Arg Ala Val Pro Val Cys Gly His Leu Gly Leu Thr Pro Gln Ser Val  
130 135 140

Asn Ile Phe Gly Gly Tyr Lys Val Gln Gly Arg Gly Asp Glu Ala Gly  
145 150 155 160

Asp Gln Leu Leu Ser Asp Ala Leu Ala Leu Glu Ala Ala Gly Ala Gln  
165 170 175

Leu Leu Val Leu Glu Cys Val Pro Val Glu Leu Ala Lys Arg Ile Thr  
180 185 190

Glu Ala Leu Ala Ile Pro Val Ile Gly Ile Gly Ala Gly Asn Val Thr  
195 200 205

Asp Gly Gln Ile Leu Val Met His Asp Ala Phe Gly Ile Thr Gly Gly  
210 215 220

His Ile Pro Lys Phe Ala Lys Asn Phe Leu Ala Glu Thr Gly Asp Ile  
225 230 235 240

Arg Ala Ala Val Arg Gln Tyr Met Ala Glu Val Glu Ser Gly Val Tyr  
245 250 255

Pro Gly Glu Glu His Ser Phe His  
260

<210> 8  
 <211> 267  
 <212> PRT  
 <213> Schizosaccharomyces pombe

<400> 8

Met	Ser	Leu	Lys	Gln	Ile	Thr	Ile	Ser	Thr	Leu	Arg	Gln	Trp	Lys	Leu
1				5					10					15	
Ala	Asn	Lys	Lys	Phe	Ala	Cys	Ile	Thr	Ala	Tyr	Asp	Ala	Ser	Phe	Ser
			20					25					30		
Arg	Leu	Phe	Ala	Glu	Gln	Gly	Met	Pro	Val	Met	Leu	Val	Gly	Asp	Ser
		35					40					45			
Leu	Gly	Met	Thr	Ala	Gln	Gly	His	Ser	Thr	Thr	Leu	Pro	Val	Ser	Val
	50					55					60				
Glu	Asp	Ile	Ala	Tyr	His	Thr	Lys	Ser	Val	Arg	Arg	Gly	Ala	Pro	Asn
65					70					75					80
Arg	Leu	Leu	Met	Ala	Asp	Leu	Pro	Phe	Met	Ser	Tyr	Ser	Thr	Trp	Glu
				85					90					95	
Asp	Ala	Cys	Lys	Asn	Ala	Ala	Thr	Val	Met	Arg	Ala	Gly	Ala	Asn	Ile
			100					105					110		
Val	Lys	Ile	Glu	Gly	Gly	Gly	Asn	Trp	Ile	Phe	Glu	Ile	Val	Gln	Arg
	115						120					125			
Leu	Thr	Glu	Arg	Ser	Val	Pro	Val	Ala	Gly	His	Leu	Gly	Leu	Thr	Pro
	130					135					140				
Gln	Ser	Val	Asn	Ile	Phe	Gly	Gly	Tyr	Lys	Ile	Gln	Gly	Arg	Glu	Gln
145				150					155						160
Ser	Ala	Ala	Ala	Arg	Leu	Ile	Glu	Asn	Ala	Gln	Gln	Leu	Glu	Lys	Phe
				165					170					175	
Gly	Ala	Gln	Leu	Leu	Val	Leu	Glu	Cys	Ile	Pro	Glu	Ser	Leu	Ala	Glu
			180					185					190		
Gln	Ile	Thr	Lys	Thr	Ile	Ser	Ile	Pro	Thr	Ile	Gly	Ile	Gly	Ala	Gly
	195					200						205			
Lys	His	Thr	Asp	Gly	Gln	Ile	Leu	Val	Met	His	Asp	Ala	Leu	Gly	Ile
	210				215						220				
Thr	Gly	Gly	Arg	Pro	Pro	Lys	Phe	Ala	Lys	Asn	Phe	Leu	Ser	Gly	Ala
225					230					235					240
Gly	Asp	Ile	Arg	Thr	Ala	Ile	Gln	Arg	Tyr	Ile	Tyr	Glu	Val	Glu	Gln
				245					250					255	
Gly	Leu	Tyr	Pro	Ala	Glu	Glu	His	Ser	Phe	Gln					
			260					265							

<210> 9  
 <211> 349  
 <212> PRT  
 <213> *Aspergillus nidulans*

<400> 9  
 Met Thr Phe Leu Arg Ile Ala Thr Lys Arg Ala Ile Tyr Leu His Arg  
   1                  5                  10                  15  
 Pro Ala Asn Pro Ala Leu Pro Thr Ser Ser Ile Leu Pro Val Leu His  
                   20                  25                  30  
 Ser Thr Asn Val Ala Thr Arg Val Pro Ser Pro Cys Ala Ile Arg His  
           35                  40                  45  
 Ser Ser His Ser Pro Leu Gly Ala Ala Gln Ala Asn Pro Arg Lys Lys  
   50                  55                  60  
 Val Thr Met Gln Thr Leu Arg Asn Leu Tyr Lys Lys Gly Glu Pro Ile  
   65                  70                  75                  80  
 Thr Met Leu Thr Ala His Asp Phe Pro Ser Ala His Val Ala Asp Ala  
                   85                  90                  95  
 Ala Gly Met Asp Met Ile Leu Val Gly Asp Ser Leu Ala Met Val Ala  
           100                  105                  110  
 Leu Gly Met Gln Asp Thr Ser Glu Val Thr Leu Asp Asp Met Leu Val  
   115                  120                  125  
 His Cys Arg Ser Val Ala Arg Ala Ala Gln Ser Ala Phe Thr Val Ser  
   130                  135                  140  
 Asp Leu Pro Met Gly Ser Tyr Glu Val Ser Pro Glu Gln Ala Leu Gln  
   145                  150                  155                  160  
 Ser Ala Ile Arg Ile Val Lys Glu Gly Arg Val Gln Gly Val Lys Leu  
           165                  170                  175  
 Glu Gly Gly Glu Glu Met Ala Pro Ala Ile Lys Arg Ile Thr Thr Ala  
           180                  185                  190  
 Gly Ile Pro Val Val Gly His Ile Gly Leu Thr Pro Gln Arg Gln Asn  
   195                  200                  205  
 Ala Leu Gly Gly Phe Arg Val Gln Gly Lys Ser Thr Thr Asp Ala Leu  
   210                  215                  220  
 Lys Leu Leu Lys Asp Ala Leu Ala Val Gln Glu Ala Gly Ala Phe Met  
   225                  230                  235                  240  
 Ile Val Ile Glu Ala Val Pro Pro Glu Ile Ala Ser Ile Val Thr Gln  
           245                  250                  255  
 Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Cys Ser  
   260                  265                  270

Gly Gln Val Leu Val Gln Ile Asp Met Thr Gly Asn Phe Pro Pro Gly  
 275 280 285

Arg Phe Leu Pro Lys Phe Val Lys Gln Tyr Ala Asn Val Trp Asn Glu  
 290 295 300

Ala Leu Gln Gly Ile Gln Gln Tyr Arg Glu Glu Val Lys Ser Arg Ala  
 305 310 315 320

Tyr Pro Ala Glu Gln His Thr Tyr Pro Ile Pro Lys Glu Glu Leu Val  
 325 330 335

Glu Phe Gln Lys Ala Val Asp Glu Leu Pro Glu Glu Lys  
 340 345

<210> 10

<211> 347

<212> PRT

<213> Arabidopsis thaliana

<400> 10

Met Ala Ser Ser Leu Thr Arg Asn Cys Ser Arg Phe Ser Lys Ala Ile  
 1 5 10 15

Ser Val Arg Phe Met Ser Asn Leu Pro Glu Asn Thr Val Tyr Gly Gly  
 20 25 30

Pro Lys Pro Gln Asn Pro Asn Gln Arg Val Thr Leu Thr His Leu Arg  
 35 40 45

Gln Lys His Arg Arg Gly Glu Pro Ile Thr Val Val Thr Ala Tyr Asp  
 50 55 60

Tyr Pro Ser Ala Val His Leu Asp Thr Ala Gly Ile Asp Val Cys Leu  
 65 70 75 80

Val Gly Asp Ser Ala Ser Met Val Val His Gly His Asp Thr Thr Leu  
 85 90 95

Pro Ile Ser Leu Asp Glu Met Leu Val His Cys Arg Ala Val Ala Arg  
 100 105 110

Gly Ala Lys Arg Pro Leu Leu Val Gly Asp Leu Pro Phe Gly Thr Tyr  
 115 120 125

Glu Ser Ser Ser Ser Gln Ala Val Asp Thr Ala Val Arg Val Leu Lys  
 130 135 140

Glu Gly Gly Met Asp Ala Ile Lys Leu Glu Gly Gly Ser Ala Ser Arg  
 145 150 155 160

Ile Thr Ala Ala Lys Ala Ile Val Glu Ala Gly Ile Ala Val Ile Gly  
 165 170 175

His Val Gly Leu Thr Pro Gln Ala Ile Ser Val Leu Gly Gly Phe Arg  
 180 185 190

Pro Gln Gly Arg Asn Ile Ala Ser Ala Val Lys Val Val Glu Thr Ala  
195 200 205

Met Ala Leu Gln Glu Ala Gly Cys Phe Ser Val Val Leu Glu Cys Val  
210 215 220

Pro Pro Pro Val Ala Ala Ala Ala Thr Ser Ala Leu Lys Ile Pro Thr  
225 230 235 240

Ile Gly Ile Gly Ala Gly Pro Phe Cys Ser Gly Gln Val Leu Val Tyr  
245 250 255

His Asp Leu Leu Gly Met Met Gln His Pro His His Ala Lys Val Thr  
260 265 270

Pro Lys Phe Cys Lys Gln Tyr Ala Asn Val Gly Glu Val Ile Asn Lys  
275 280 285

Ala Leu Met Glu Tyr Lys Glu Glu Val Ser Lys Lys Val Phe Pro Gly  
290 295 300

Pro Ser His Ser Pro Tyr Lys Ile Thr Ala Ser Glu Leu Asp Gly Phe  
305 310 315 320

Leu Thr Glu Leu Gln Lys Leu Gly Phe Asp Lys Ala Ala Ser Ala Ala  
325 330 335

Ala Leu Ala Ala Glu Asn Met Glu Pro Ser Lys  
340 345

<210> 11

<211> 312

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 11

Met Asn Ile Met Lys Arg Gln Leu Cys Thr Ser Ser Lys Arg Phe Phe  
1 5 10 15

Ser Thr Ala Lys Asn Val Val Lys Tyr Asn Thr Ile Gln Asp Ile Arg  
20 25 30

Asn Lys Tyr Phe Thr Gly Thr Pro Leu Ser Met Cys Thr Ala Tyr Asp  
35 40 45

Phe Ile Thr Ala Thr Trp Val Asn Lys Ala Asn Cys Asp Leu Leu Leu  
50 55 60

Val Gly Asp Ser Leu Ala Met Thr Ser Leu Gly Tyr Asp Ser Thr Ile  
65 70 75 80

Thr Leu Ser Leu Asn Glu Phe Lys Tyr His Val Ala Ser Val Cys Arg  
85 90 95

Ala Glu Gly Ser Ser Met Val Val Val Asp Met Pro Phe Gly Thr Phe  
100 105 110

Glu Ser Gly Ile Ser Asp Gly Leu Lys Asn Ala Ile Asp Ile Met Lys  
           115                                  120                                  125  
 Leu Asp Ser Lys Val Thr Ser Val Lys Val Glu Val Gly Ser Tyr Thr  
           130                                  135                                  140  
 Lys Asp Lys Tyr Ala Met Lys Phe Ile Glu Glu Leu Cys Ser Arg Gly  
           145                                  150                                  155                                  160  
 Ile Pro Val Met Ala His Ile Gly Leu Thr Pro Gln Lys Val His Ser  
                                   165                                  170                                  175  
 Leu Gly Gly Tyr Lys Val Gln Gly Ser Lys Ser Leu Leu Gln Met Gln  
                                   180                                  185                                  190  
 Glu Leu Tyr Glu Thr Ala Met Gln Leu Gln Lys Ile Gly Cys Trp Ser  
           195                                  200                                  205  
 Ile Leu Ile Glu Cys Val Pro His Lys Met Ala Gln Phe Ile Thr Ser  
           210                                  215                                  220  
 Lys Leu Ser Val Pro Thr Ile Gly Ile Gly Ala Gly Asn Gly Thr Ser  
           225                                  230                                  235                                  240  
 Gly Gln Val Leu Val Ile Ser Asp Leu Leu Gly Met Gln Gly Asp Ser  
                                   245                                  250                                  255  
 Val Pro Lys Phe Val Lys Gln Ala Val Asn Met Thr Asp Ile Ala Thr  
                                   260                                  265                                  270  
 Gln Gly Leu Lys Glu Tyr Ile Ala Ser Val Glu Asp Arg Thr Phe Pro  
           275                                  280                                  285  
 Glu Arg Gly Thr His Thr Phe Lys Val Lys Glu Asp Leu Trp Asn Glu  
           290                                  295                                  300  
 Phe Leu Ser Ser Ile Asn Glu Lys  
           305                                  310

<210> 12

<211> 281

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus

<220>

<221> SITE

<222> 1..4, 6..8, 10..22, 27..29, 31..39, 41, 50..52, 54..56

<223> Xaa is uncertain

<220>

<221> SITE

<222> 59, 62..64, 66, 67, 69..71, 73, 76..81, 83, 88, 89

<223> Xaa is uncertain



<220>  
 <221> SITE  
 <222> 91..96, 97..100, 102, 103, 105..108, 110..113, 120..133  
 <223> Xaa is uncertain

<220>  
 <221> SITE  
 <222> 135..138, 140, 142, 145, 151..155, 163, 165..171  
 <223> Xaa is uncertain

<220>  
 <221> SITE  
 <222> 173..175, 177, 179..181, 185, 186, 191, 194, 195  
 <223> Xaa is uncertain

<220>  
 <221> SITE  
 <222> 198..200, 202..205, 208, 215..217, 224, 225, 227, 228  
 <223> Xaa is uncertain

<220>  
 <221> SITE  
 <222> 230..242, 246, 248..258, 260..262, 264..266, 268..271  
 <223> Xaa is uncertain

<220>  
 <221> SITE  
 <222> 274..277, 279..281  
 <223> Xaa is uncertain

<400> 12  
 Xaa Xaa Xaa Xaa Thr Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
   1                  5                  10                  15  
 Xaa Xaa Xaa Xaa Xaa Xaa Thr Ala Tyr Asp Xaa Xaa Xaa Ala Xaa Xaa  
                   20                  25                  30  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Xaa Leu Val Gly Asp Ser Leu Gly  
                   35                  40                  45  
 Met Xaa Xaa Xaa Gly Xaa Xaa Xaa Thr Leu Xaa Val Thr Xaa Xaa Xaa  
       50                  55                  60  
 Ile Xaa Xaa His Xaa Xaa Xaa Val Xaa Arg Gly Xaa Xaa Xaa Xaa Xaa  
   65                  70                  75                  80  
 Xaa Leu Xaa Asp Leu Pro Phe Xaa Xaa Tyr Xaa Xaa Xaa Xaa Xaa Xaa  
                   85                  90                  95  
 Ala Xaa Xaa Xaa Ala Xaa Xaa Val Xaa Xaa Xaa Xaa Ala Xaa Xaa Xaa  
                   100                  105                  110  
 Xaa Val Lys Ile Glu Gly Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
   115                  120                  125  
 Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Val Xaa Val Xaa Gly His  
   130                  135                  140

Xaa Gly Leu Thr Pro Gln Xaa Xaa Xaa Xaa Xaa Gly Gly Tyr Lys Val		
145	150	155 160
Gln Gly Xaa Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Ala		
	165	170 175
Xaa Ala Xaa Xaa Xaa Ala Gly Ala Xaa Xaa Leu Val Leu Glu Xaa Val		
	180	185 190
Pro Xaa Xaa Leu Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa Xaa Ile Pro Xaa		
	195	200 205
Ile Gly Ile Gly Ala Gly Xaa Xaa Xaa Asp Gly Gln Ile Leu Val Xaa		
	210	215 220
Xaa Asp Xaa Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
225	230	235 240
Xaa Xaa Pro Lys Phe Xaa Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa		
	245	250 255
Xaa Xaa Ala Xaa Xaa Xaa Tyr Xaa Xaa Xaa Val Xaa Xaa Xaa Xaa Tyr		
	260	265 270
Pro Xaa Xaa Xaa Xaa His Xaa Xaa Xaa		
	275	280